

10 30 50
GTGAGATGGTGTCTTCATGAATTCCTCCCAACAAGAGCCAAGCTCTCCATCTAGTGGACAG
70 90 110
GGAAGCTAGCAGCAAACCTTCCCTTCACTACGAACTTCATTGCTTGGCCCAAAAGAGAG
130 150 170
TTAATTCAATGTAGACATCTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTT
190 210 230
GCATTTCATGGAGGGCAACTAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTA
250 270 290
TGCACAGGGTGAACAAGATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTAT
M D Y Q V S S P I Y D I N Y
310 330 350
TATACATCGGAGCCCTGCCCAAAATCAATGTGAAGCAAATCGCAGCCCGCTCCTGCCT
Y T S E P C P K I N V K Q I A A R L L P
370 390 410
CCGCTCTACTCACTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCATCCTCATC
P L Y S L V F I F G F V G N M L V I L I
430 450 470
CTGATAAACTGCCAAAGGCTGGAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATC
L I N C Q R L E S M T D I Y L L N L A I
490 510 530
TCTGACCTGTTTTCTTCTTACTGTCCCTTCTGGGCTCACTATGCTGCCGCCAGTGG
S D L F F L L T V P F W A H Y A A A Q W
550 570 590
GACITTTGAAATACAATGTGTCAACTCTTGACAGGCTCTATTTTATAGGCTTCTTCTCT
D F G N T M C Q L L T G L Y F I G F F S
610 630 650
GGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTATCGTCCATGCTGTG
G I F F I I L L T I D R Y L A I V H A V
670 690 710
TTTGCCTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTATCACTTGGGTG
F A L K A R T V T F G V V T S V I T W V
730 750 770
GTGGCTGTGTTTGGCTCTCTCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTT
V A V F A S L P G I I F T R S Q K E G L
790 810 830
CATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAG
H Y T C S S H F P Y S Q Y Q F W K N F Q
850 870 890
ACATTAAAGATAGTCATCTTGGGGTGGTCTGCCGCTGCTTGTATGGTCATCTGCTAC
T L K I V I L G L V L P L L V M V I C Y
910 930 950
TCGGGAATCCTAAAACTCTGCTTCGGTGTGGAATGAGAAGAAGAGGCACAGGGCTGTG
S G I L K T L L R C R N E K K R H R A V

FIG.1A

970 990 1010
AGGCTTATCTTCACCATCATGATTGTTATTTCTCTTCTGGGCTCCCTACAACATTGTC
R L I F T I M I V Y F L F W A P Y N I V
1030 1050 1070
CTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGG
L L L N T F Q E F F G L N N C S S S N R
1090 1110 1130
TTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCC
L D Q A M Q V T E T L G M T H C C I N P
1150 1170 1190
ATCATCTATGCCTTTGTGCGGGAGAAGTTTCAGAACTACCTCTTAGTCTTCTTCCAAAAG
I I Y A F V G E K F R N Y L L V F F Q K
1210 1230 1250
CACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCGAGCGA
H I A K R F C K C C S I F Q Q E A P E R
1270 1290 1310
GCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGTGACAC
A S S V Y T R S T G E Q E I S V G L *
1330 1350 1370
GGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTTTTTCATACACA
1390 1410
GCCTGGGCTGGGGGTGGGGTGAAGAGGTCTTTT

FIG.1B

4 QVSSPIYDINYYTSEPCPKINVKQIAARLLPLYSLVFIFGFVGNMLVIL 53

: .::|.:| :.||.::|||:|.|||||||

18 EEVTTFFDYDY..GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVL 65

54 ILINQRLSMTDIYLLNLAI S D L F F L L T V P F W A H Y A A A Q W D F G N T M C O L 103

||||| :| :||| ||| ||| :| :| :| ||| ||| :| ||| |||

66 ILINCKKLKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKL 115

104 LTGLYFIGFFSGIFFIILLTIDRYLAIVHAFALKARTVIFGVVTSVITW 153

:||| | : : |||||||||

116 FTGLYHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGWVTSVITW 165

154 VVAVFASLPGIIFTRSQKEGLHYTCSSHFYPYSQYQFWKNFQTLKIVILGL 203

:|||:|||:|||::|||: |.:..|| : |||:|. |||

166 LVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG...WNNFHTIMRNILGL 211

204 VLP LLVMVICYSGILKTLRCRNEKKRHRVRLIFTIMIVYFLFWAPYNI 253

|||:|||||||:|||||||:

212 VLPLLIMVICYSGILKTLRCRNEKKRHRAVRVIFTIMIVYFLFWTPYN 261

254 VLLNTFQE⁺FFGLNCCSSN⁺RLDQAMQVTETLGMTHCCINPIIYAFVGEK 303

(c) [REDACTED]

262 VILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK 311

304 FRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRS...TGEQEISV 350

|| .. : : : : || : : | .. : .. | : : . | | : : . : : : | :

312 FRSLFHIALGCRIA.PLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

351 G 351

1

361 G 361

FIG. 2

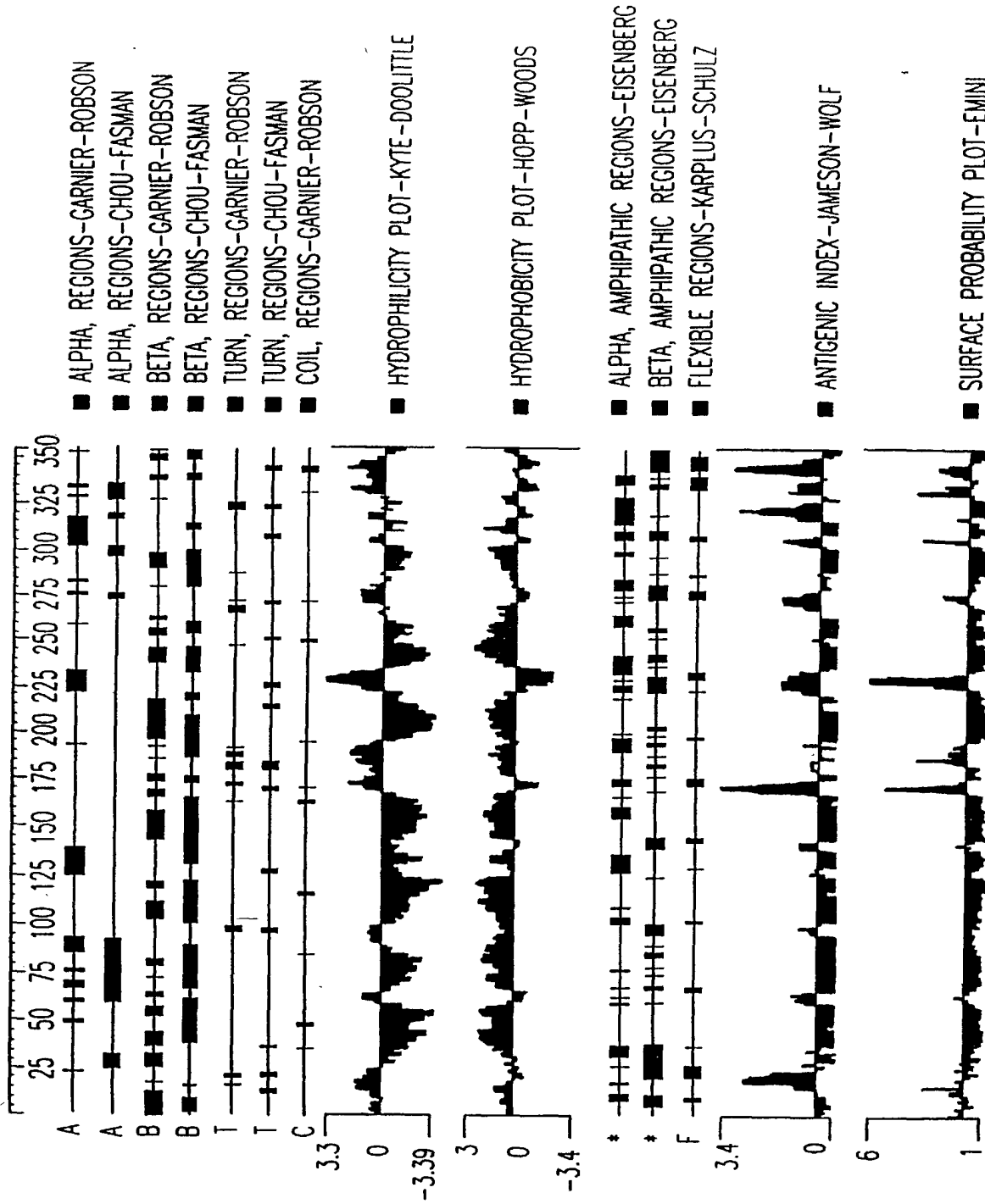


FIG.3

Anti-CCR5 1D8 VH Sequence

1 CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC
 1 Q V Q L Q E S G P G L V K P S E T L S L

 61 ACC TGC ACT GTC TCT GGT GGC TCC ATC AGT AGT TTC TAC TGG AGC TGG ATC CGG CAG CCC
 21 T C T V S G G S I S S F Y W S W I R Q P

 121 GCC GGG AAG GGA CTG GAC TGG ATT GGG CGT ATC TAT ACC AGC GGG AAC ACC AAC TAC AAC
 41 A G K G L D W I G R I Y T S G N T N Y N

 181 CCC TCC CTC AAG AGT CGA GTC ACC ATG TCA GTA GAC ACG TCC AAG AAC CGG TTC TCC CTG
 61 P S L K S R V T M S V D T S K N R F S L

 241 AAA CTG AGC TCT GTG ACC GCC GCG GAC ACG GCC GTG TAT TAC TGT GCG AGA GAT CGG GGC
 81 K L S S V T A A D T A V Y Y C A R D R G

 301 AGC AGC TGG TAC CCC GAT GCT TTT GAT ATC TGG GGC CAA GGG ACA ATG GTC ACC GTC TCC
 101 S S W Y P D A F D I W G Q G T M V T V S

 361 TCA
 121 S

Anti-CCR5 1D8 VK Sequence

1 GAT ATT GTG TTG ACG CAT TCT CCA GGC ACC CTG TCT TTG TCT CCA GGG GAA AGA GCC ACC
 1 D I V L T H S P G T L S L S P G E R A T

 61 CTC TCC TGC AGG GCC AGT CAG CGT GTT ACC AGC AGC TGC TTA GCC TGG TAC CAG CAG AAA
 21 L S C R A S Q R V T S S C L A W Y Q Q K

 121 CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GGT ACA TCC AGC AGG GCC ACT GGC ATC CCA
 41 P G Q A P R L L I Y G T S S R A T G I P

 181 GAC AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGA CTG GAG
 61 D R F S G S G S G T D F T L T I S R L E

 241 CCT GAA GAT TTT GCA GTG TAT TAC TGT CAG CAG TAT GTT AGC TCA CCT CTC ACC TTC GGC
 81 P E D F A V Y Y C Q Q Y V S S P L T F G

 301 CAA GGG ACA CGA CTC GAG ATC AAA CGT
 101 Q G T R L E I K R

FIG.4

Anti-CCR5 3C9 VH

1 GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTA AAG TCT GGG GGG TCC CTT AGA CTC 60
 1 E V Q L V E S G G G L V K S G G S L R L 20

CDR1

61 TCC TGT GCA GCC TCC GGA TTC ACT TTC AGT AAC GCC TGG ATG ACC TGG GTC CGC CAG GCT 120
 21 S C A A S G F T F S N A W M T W V R Q A 40

CDR2

121 CCA GGG AAG AGG CTG GAG TGG GTT GGC CGT ATT AAA AGC AAT GCT GAT GGT GGG TCA ACA 180
 41 P G K R L E W V G R I K S N A D G G S T 60

181 GAC TAC GCT GCA CCC GTG AAA GGC AGA TTC ACC ATC TCA AGA GAT GAT TCA AAA AAC ACG 240
 61 D Y A A P V K G R F T I S R D D S K N T 80

241 CTG TAT CTG CAA ATG AAC AGC CTG AAA ACC GAG GAC ACA GCC GTG TAT TAC TGT AAC ACA 300
 81 L Y L Q M N S L K T E D T A V Y Y C N T 100

CDR3

301 GAT AAG GGT GGG AGC TAC CCC TAC TAC TAC TAC GGT ATG GAC GTC TGG GGC CAA GGG ACC 360
 101 D K G G S Y P Y Y Y Y G M D V W G Q G T 120

361 ACG GTC ACC GTC TCC TCA G 379

121 T V T V S S 127

Anti-CCR5 3C9 VK

1 GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC 60
 1 D I Q M T Q S P S S L S A S V G D R V T 20

CDR1

61 ATC ACT TGC CCG GCA AGT CAG GGC ATT AGA AAT GAT TTA GGC TGG TAT CAG CAG AAA CCA 120
 21 I T C R A S Q G I R N D L G W Y Q Q K P 40

CDR2

121 GGG AAA GCC CCT AAG CGC CTG ATC TAT GAT GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA 180
 41 G K A P K R L I Y D A S S L Q S G V P S 60

181 AGG TTC AGC GGC AGT GGA TCT GGG ACA GAA TTC ACT CTC ACA ATC AGC AGC CTG CAG CCT 240
 61 R F S G S G S G T E F T L T I S S L Q P 80

CDR3

241 GAA GAT TTT GCA ACT TAT TAC TGT CTA CAG CAT AAT AGT TAC CCA TTC ACT TTC GGC CCT 300
 81 E D F A T Y Y C L Q H N S Y P F T F G P 100

301 GGG ACC AAA GTG GAT ATC AAA CGA 324

101 G T K V D I K R 108

FIG.5

Appl No 10/067,800, Filed February 8, 2002

Dkt. No 1488 1150001, Group Art Unit. 1642

Inventors Roschke *et al.*, Tel 202/371-2600

Title Human G-protein Chemokine Receptor (CCR5)

HIDGNR10

Anti-CCR5 9E6 VH

1 GAG GTG CAG CTG GTG GAG TCT GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC 60
 1 E V Q L V E S G P G L V K P S E T L S L 20

CDR1

61 ACC TGC ACT GTC TCT GGT GGC TCC ATC AGT AGT TAC TAC TGG AGC TGG ATC CGG CAG CCC 120
 21 T C T V S G G S I S S Y Y W S W I R Q P 40

CDR2

121 CCA GGG AAG GGA CTG GAG TGG ATT GGG TAT ATC TAT TAC AGT GGG AGC ACC AAC TAC AAC 180
 41 P G K G L E W I G Y I Y Y S G S T N Y N 60

181 CCC TCC CTC AAG AGT CGA GTC ACC ATA TCA GTA GAC ACG TCC AAG AAC CAG TTC TCC CTG 240
 61 P S L K S R V T I S V D T S K N Q F S L 80

241 AAG CTG AGC TCT GTG ACC GCT GCG GAC ACG GCC GTG TAT TAC TGT GCG AGA GAT GTC ATG 300
 81 K L S S V T A A D T A V Y Y C A R D V M 100

CDR3

301 CAG CAG CCG GTA CCG GGT TAC TAC TAC TAC TAC GGT ATG GAC GTC TGG GGC CAA GGA ACC 360
 101 Q Q P V R G Y Y Y Y Y G M D V W G Q G T 120

361 CTG GTC ACC GTC TCC TCA 378

121 L V T V S S 126

Anti-CCR5 9E6 VK

1 GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTG TCT TTG TCT CCA GGG GAA AGA GTC ACC 60
 1 E I V L T Q S P G T L S L S P G E R V T 20

CDR1

61 CTC TCC TGC AGG GCC AGT CAG AGA GTT AGC AAC AGC TAC TTA GCC TGG TAC CAG CAG AAA 120
 21 L S C R A S Q R V S N S Y L A W Y Q Q K 40

CDR2

121 CCT GGC CAG GCT CCC AGG TTC CTC ATC TAT GGT GTA TCC AGC AGG GCC ACT GGC ATC CCA 180
 41 P G Q A P R F L I Y G V S S R A T G I P 60

181 GAC AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGA CTG GAG 240
 61 D R F S G S G S G T D F T L T I S R L E 80

CDR3

241 CCT GAA GAT TTT GCA GTG TAT TAC TGT CAG CAG TAT GGT AGT TCA CCG TGG ACG TTC GGC 300
 81 P E D F A V Y Y C Q Q Y G S S P W T F G 100

301 CAA GGG ACC AAG GTG GAA ATC AAA CGA 327

101 Q G T K V E I K R 109

FIG.6